

Figure 1A

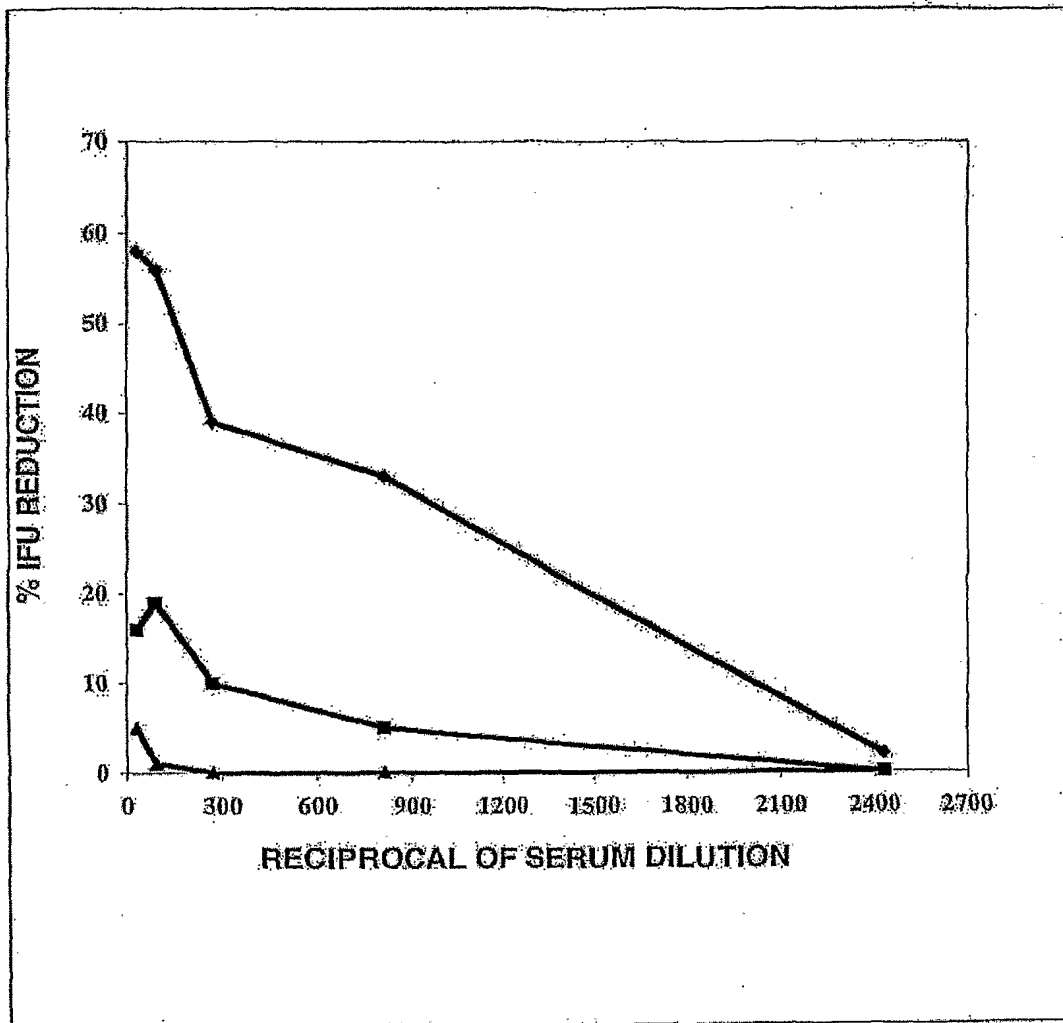
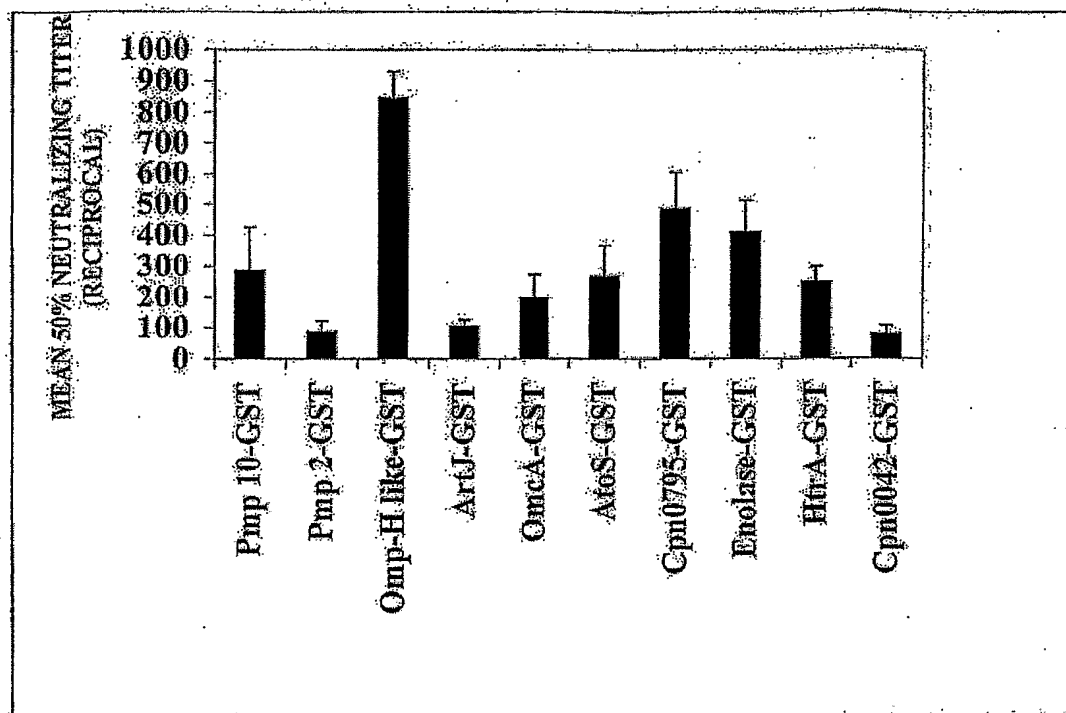


Figure 1B



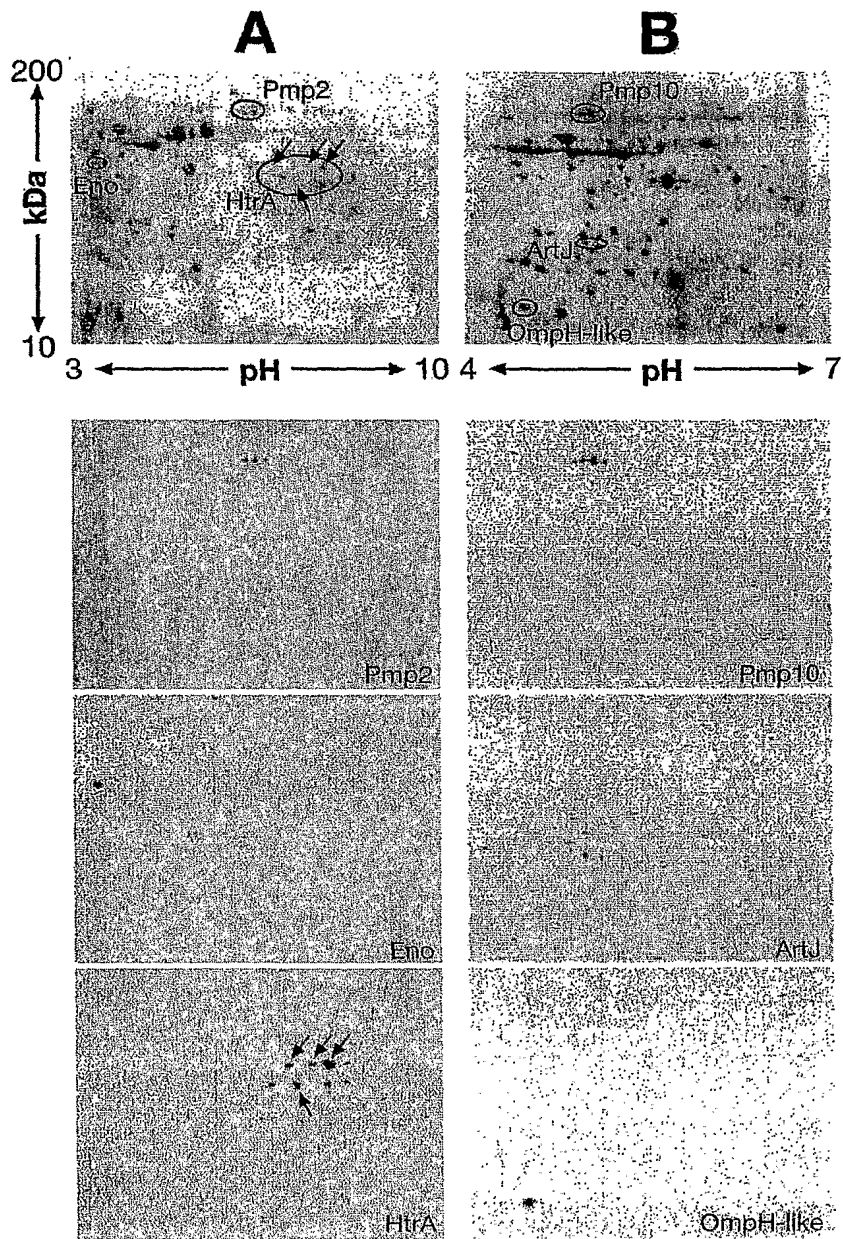


Figure 2

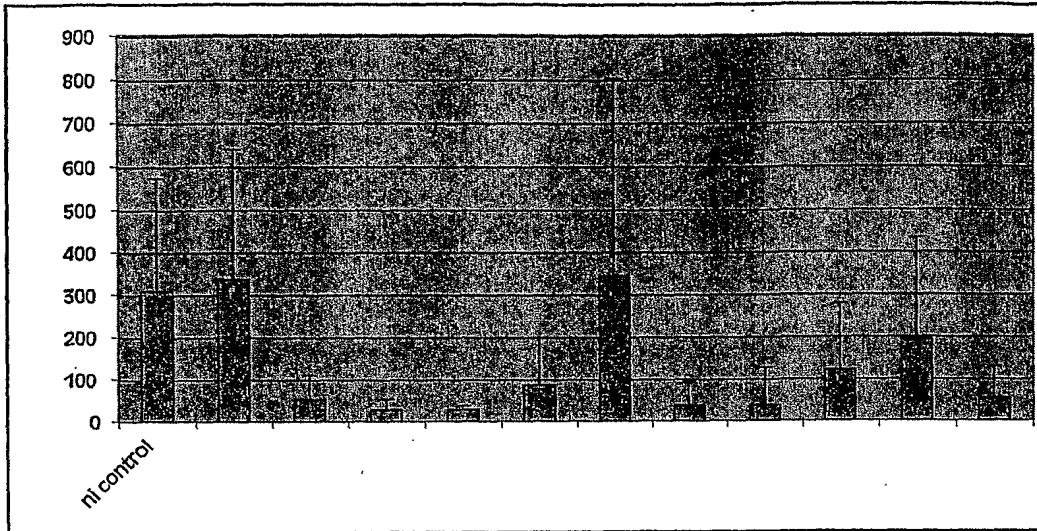


Figure 3. Mean numbers of *C.pneumoniae* IFU recovered from equivalent spleen samples from immunized and mock-immunized hamsters following a systemic challenge. Standard deviation values are shown above the bars. Antigens which induced significant protection are highlighted with an asterisk above the corresponding bar. All antigens were delivered in Freund's adjuvant. n.i. = non immunized controls

Figure 4

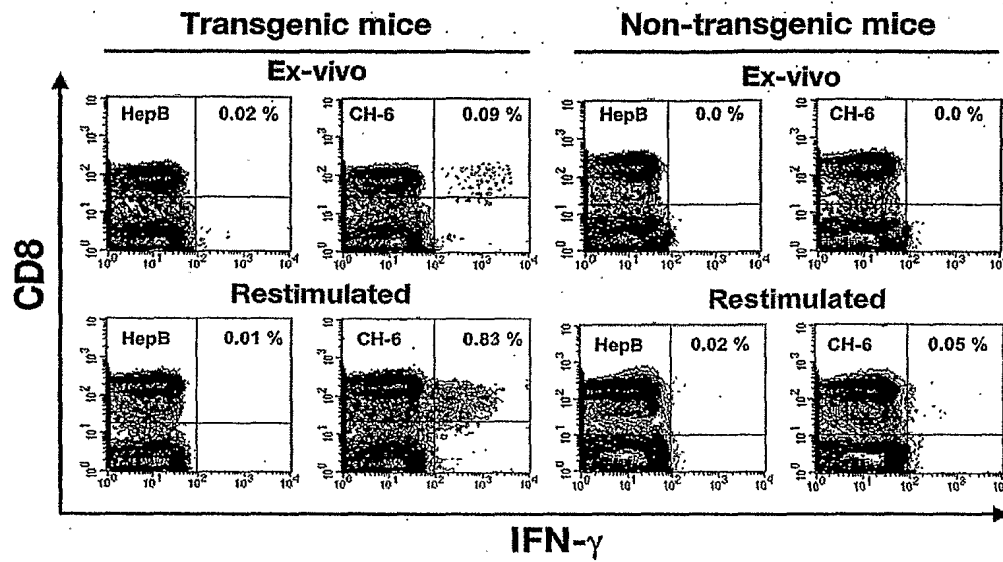
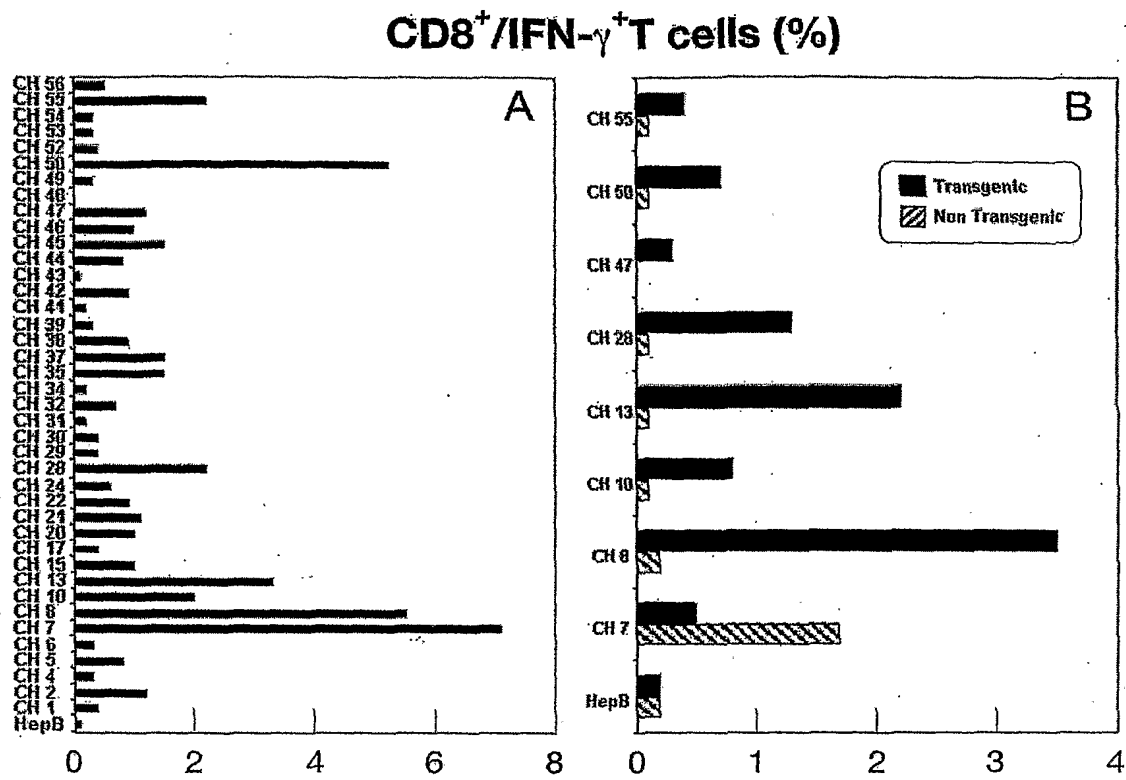
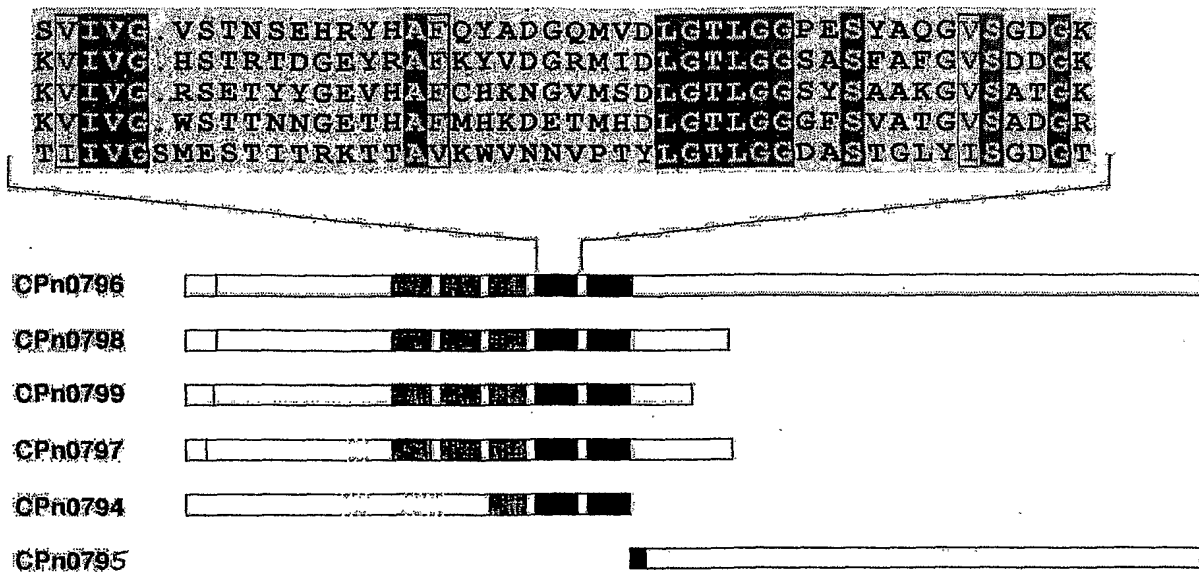


Figure 5





This Alignment shows a new family of proteins expected to constitute a system of antigens probably delivered on the Cpn surface or secreted by a type V (autotransporter) secretion mechanism

Fig. 6

N-terminal alignment

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Cpn0796      MQPCLNMSIVRNSALPLPCLSRSETFFKKVRSHMKFMKVLTPWIYRKDLWVTAFLLLTAIPG 60
Cpn0798      -----MKKTCCQNYRSIGVVFS-----VVLFVLTQT- 27
Cpn0799      -----MAAIKQILRSMLSQSSLMVLFSLYSLSG-----YCYVITDKPEDDFHSSSAVK 49
Cpn0797      -----MSKKIKVLGHLTLC'FLFRGVLCAAALSN-----IGYASTSQESPQKSIED 46
Cpn0794      -----MSLYQKWWSQLKKSLCYSTVAA-----LIFMIPSQE 32

Cpn0796      SFAHTLVLDIAGEPRH-AAQATGVSGDGKMKVPPDDPF--TVGFQYIDGHLQPLEAVR 119
Cpn0798      LFAGHFIDIG-TSGL-YSWARGVSGDGRVYEGGN----KYVDGEKFLLEGLV---- 78
Cpn0799      WDHWGKTTLSRLSNK-KASAKAVSGTGATTFIKDTWSRTYRWNYWGTEKELPTSSWV-- 108
Cpn0797      WKGYTFTDLELLSKEGWSEAHAVSGNGSRASGAGQGSVTIWESHLIK----- 103
Cpn0794      SFADSLIDLNLGLDP----- 62

Cpn0796      PQCSVYPNGITPDGTVGCTNYAIGMGSVKWNKGSEKPLPDITLD----SVASAVSADGR 179
Cpn0798      PRSEALVFKASYDGSNAGIS-DQDPSCRKWNNGAVVIFSEGMQ----SFAEGVSSDGR 137
Cpn0799      KKS--KATGISSDGSNAGIVENELSQSFATWKNNEYLIPST-WAVQ----SKAYGISSDGS 165
Cpn0797      --EASSAEGISKDGSNAGVSDTREGYTAVFDGRDKATYS-----VARGVSGDGS 162
Cpn0794      ----SVECLSGDGAFSGYFTKAGSTPVEYQPFKYDVSKKTFITLSVETANQSGYAYGISYDGT 107

Cpn0796      --SGNRNINLGAS---VWKWEDD-VITQLPSLPDAM-NACVNGISSDGSITVGMVDV 233
Cpn0798      TVGCLYSDDTETN---FKWDET-GMVVLPNLPEDR-HSCAWDASEDGSITVGDAMGS 192
Cpn0799      TVGGS-AKDAWSRT---FKWTGH-EAQVLP-VGWAV-KSVANSVSANGSITVGSVQDA 218
Cpn0797      TVGVSATARGEDYGVQGVKWEKG-KIKQLKLLPQGL-WSEANAISEDGTVVGRGEIS 220
Cpn0794      TVGTGCSLGAGKYN---GAKWSADTPTLTGTTGGTSHTEARAISKDTQVTEGFSYDA 163

Cpn0796      SWRNTQWIG--DQLSVIT--SVASAISTDGTIVGSGSE-NADSQTAYKN 288
Cpn0798      EEIAKQWKD--GEQHLASNPAKR-SSAHAVSKDGSFTVGEFT-SEENEVYVHN 248
Cpn0799      SGILYKWEK--NTITHLYS-AIAKAVSNNGKVVRSE-TYYGEVCHKN 273
Cpn0797      RNHIVKWNK--NAVYSV--ASAEAISANGKVTVGWST-TNNGETMHKD 275
Cpn0794      SGQPKQWASGATTVTOADSGSRSSYAYATSDGTITVGSMESTITRKTWKVN 223

Cpn0796      GVSSTFYSLAHAVSSDGSITVGVVS-----TNSEHRYQYADGOV 343
Cpn0798      GVKKDYSVATGVSRDGVVGHHS-----TRIDGEYKYVDGR 303
Cpn0799      GVSSTSYSAAGVSAIGKVVGMS-----TTANGKLYVGGRIEYSW 328
Cpn0797      ETTHGFSVATGVSAIGRAIVGFS-----AVKTGETIYAEGE 330
Cpn0794      NVPTVADASTGLYISGDETVMGAANTATVTNGNOESMYKDNOK----- 277
Cpn0795      ----- 327

Cpn0796      PESYAQGVSGDGKVLVQRAQVPSGDWLCPPQAPSPAPVHGGSTVVTSONPRGMVDIN 403
Cpn0798      SASFAFGVSDDGKTVGKFETELGECIYLLD----- 337
Cpn0799      KEACANAVSIDGETVGVQSE----- 349
Cpn0797      EEARVFDISSGNDTTSIKTDAGAERAYLFHIHK----- 365
Cpn0795      TSSTAKTVSPDGKVLMSRSQIADGSWMCHTDFSSNNVLFDLDN

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FIG. 7

Cpn0796

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1  MKFMKVLTPW IYRKDLWVTA FLLTAIPGSF AHTLV DIA  TGV
51  SGDGRIVIGM KVPDDPFAIT VGFOYIDGHL QPLEAVRPQC SVYPNGITPD
101 GTVIVGTNYA ICMGSVAVKW VNGKVSELPN LPDTLDSVAS AVSADGRVIG
151 GNRNINLGAS VAVKWEDDVI TQLPSLPDAM NACVNGISSD GSIIVGTMVD
201 VSWRNTAVQW IGDQLSVIGT LGGTTSVASA ISTDGTVIVG GSENADSQTH
251 AYAYKNGVMS DICTLGGFYS LAHAVSSDGS VIVGVSTNSE HRYHAFOYAD
301 GOMVDLGLTG GPESYAQGVN GDGKVIVGRA QVPSGDWHAF LCPFQAPSPA
351 PVHGGSTVVT SQNPRGMVDI NATYSSLKNS QQQLQRLLIQ HSAKVESVSS
401 GAPSFTSVKG AISKQSPAVQ NDVOKGTFLS YRSQVHGNVO NQQLLTGAFM
451 DWKLASAPKC GFKVALHYGS QDAIVERAAL PYTEOGLGSS VLSGFGGQVQ
501 GRYDFNLGET VVLQPFMGIO VLHLSREGYS EKNVRFVPSY DSVAYSATS
551 FMGAHVFAFL SPKMSTAATI GVERDLNSHI DEFKGSVSAM GNFVLENSTV
601 SVLRPFASLA MYYDVRRQQQL VTLNVMMNQO PLTGTLNLVS QSSYNLSF

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Leader peptide	1-31
Or, alternatively:	
Leader peptide 2	1-47
b-propeller domain	32-342
Or, alternatively:	
b-propeller domain2	48-342
linker region	343-364
helix	365-385
beta barrel	386-648

FIG. 8

Alignment of the C-terminal (beta barrell) domains of the proteins encoded by the
C.pneumoniae genes Cpn0795 (7016) and Cpn0796 (7107)

```

7106 -----TSSTAKTVSPDGKVLICRSQIADGSWHAFMCHTDFSSNNVLFDLDN
7107 YADGQ-----PESYAQGVSGDGKVLICRAQVPSPGDWHAFLCFFQAPSPAPVHGGST
      * *****... * : * * *****:***:..*.....* : . * :...

7106 TYKTLRENGRQLNSIFNLQNMMLQRASDHEFTEFGRSNIALGAGLYVNALQNLPNLAQ
7107 VVTSQ--NPRGMVDINATYSSSLKNSQQQLQRLLIQHSKAKVESVSSGAPSFSTSVKGAISKQ
      . . : . * * : . * . : : . : : : : * . . . . . : : . : : *

7106 YFGIAYKIRPKYRLGVFLDHNFFSSHVPNNFNVSHNRLWMGAFIGWQSDALGSSVKVSFG
7107 SP----AVQNDVQKGTFLSYRSQVHG----NVQNQQLLTGAFMDWKLASAPKCGFKVALH
      . : : : . : . : *..... . * . . . ***** * : * .....

7106 YGKQKATITREQLNTEAGSGESHFEGVAAQIEGRYKSLGSHVVRVQPFLLGLQFVHITRK
7107 YGSQDALVERAALPYTEQGLGSSVLSGFGGQVQGRYDFNLGETVVLQPFMGIQVLHLSRE
      **.*. * : * * * * * * : ..... : ***. . ** * : ***:***:***:

7106 EYTENAVQFPVHYDPIDYSTGVVYLGIGSHIALVDSLHVGTMRMGMEQNFAAHTDRFSGSI
7107 GYSEKNVRFPVSYDSVAYSAAATSMGAHVFAASLSPKMSTAATLGVERDLNSHIDEFKGSV
      *: * : * : * * : * : . : * . : . : : * : * : * : * : * :

7106 ASIGNFVFEKLDVTHTRAFAEMRVNYELPYLQSLNLILRVNQQLQGVMGFSSDLRYALG
7107 SAMGNFVLENSTVSVLRPFASLAMYVDVRQQQLVTLVVMNQQLTGTLVSLVSQSSYNLS
      : : * : * : * : * : * : * : * : * : * : * : * : * : * :

7106 F
7107 F
      *

```

FIG. 9